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Db 841 AGGATCCGTAATATGATTAAGGATTAAGGAAATTTTATGAGATTAAGTGGAAAGGATTG 900
QY
Db 895 TTTAGAGAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 954
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 901 TACAAAACGGCTCCGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY
Db 955 CTGCTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 961 CTGCTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1005 GCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1074
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1021 GATTACCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1075 CCGTGTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1081 CCGTGTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1129 AGCAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1188
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1141 GGTAAATTTTGGAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1189 ATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1248
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1201 ACAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1249 CACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1308
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1261 CACCAAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1309 CACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1368
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1321 CATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1369 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1416
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1381 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1417 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1476
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1441 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1477 TAA 1479
QY TTT
Db 1501 TAA 1503
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Search completed: July 2, 2002, 13:38:10
Job time: 9615 sec

[illegible]

Search completed: July 1, 2002, 12:04:29
Job Time: 0:04 sec

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
 Glade, Panicoideae, Andropogoneae; Zea.

1 (bases 1 to 595)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot, V.

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plasmid: 60368 raw.D, column: 86

Location/Qualifiers

1..595

Organism="Zea mays"

Qualifier="EST"

db_xref="taxon:4577"

cdone_lib="603 - stressed root cDNA library from

Walbot/Stanford lab"

Issue_Type="Seedling"

Dev_Stage="salt stress"

Lab_Test="E coli XL Gold"

Note="Organic root, Walbot"

Seedling stressed root cDNA library from Walbot/Stanford lab"

BASE COUNT 87 a 164 c 227 g 115 t 2 others

ORIGIN

1..595

Query Match 4.78; Score 69.2; DB 9; Length 595;

Best Local Similarity 49.59; Prod No 2.1;

Mismatches 294; Conservative 0; Mismatches 290; Indels 12; Gaps 3;

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DB 48 CACGCGCGGTCGATCTCTACAGCTCCCGCTGCGGACGCGCTC 3

RESULT 8

HG321263

LOCUS

DEFINITION

2m04_03q03_K_2m04_AAFG_EVRC_cold_stressed_maize_seedlings_Zea mays

813 bp mRNA linear EST 27-FEB-2001

cdna clone Zm04_03q03, mRNA sequence.

ACCESSION HG321263

VERSION HG321263.1

KEYWORDS

EST

SOURCE

Ze mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC

Glade, Panicoideae, Andropogoneae, Zea.

REFERENCE 1 (bases 1 to 813)

AUTHORS Singh, J.A., Wakai, K., Connors, P., De Moers, A., Harris, E.T., Hartori,

J.L., Gachet, T., Robert, S., Spott, D., and Tinker, N.A.

Expressed Sequence Tags from Cold Stressed Maize Seedlings

Unpublished (2001)

COMMENT

Contact: Singh, J.A.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-Food Canada

969 Carleton Avenue, Bldg. 20, Ottawa, Ontario, K1A 0G6, Canada

Tel: (613) 759-1662

Fax: (613) 759-1701

Email: singhja@agr.ca

Location/Qualifiers

1..813

Organism="Zea mays"

Qualifier="EST"

db_xref="taxon:4577"

cdone_lib="Zm04_03q03"

Issue_Type="Leaf, crown"

Dev_Stage="Seedling"

Lab_Test="SK-XhoI-ProP; Site 1: Eco RI;

Site 2: Xba I; Lower temperature 50 °C / hour from 22 to

120 °C; bring to 50 in 1 hour from 120 °C. Leave at 50 °C 2 days

then subjected 16 hours 'high' intensity was 125 uE-1

Library prepared by in vivo mass excision from amplified

library."

BASE COUNT 174 a 296 c 215 g 104 t 24 others

ORIGIN

1..813

Query Match 4.78; Score 69.2; DB 10; Length 813;

Best Local Similarity 42.69; Prod No 2.1;

Mismatches 343; Conservative 14; Mismatches 443; Indels 6; Gaps 1;

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC

Glade, Panicoideae, Andropogoneae; Zea.

1 (bases 1 to 595)

Walbot, V.

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Email: walbot@stanford.edu

Plasmid: 60368 raw.D, column: 86

Location/Qualifiers

1..595

Organism="Zea mays"

Qualifier="EST"

db_xref="taxon:4577"

cdone_lib="603 - stressed root cDNA library from

Walbot/Stanford lab"

Issue_Type="Seedling"

Dev_Stage="salt stress"

Lab_Test="E coli XL Gold"

Note="Organic root, Walbot"

Seedling stressed root cDNA library from Walbot/Stanford lab"

BASE COUNT 87 a 164 c 227 g 115 t 2 others

ORIGIN

1..595

Query Match 4.78; Score 69.2; DB 9; Length 595;

Best Local Similarity 49.59; Prod No 2.1;

Mismatches 294; Conservative 0; Mismatches 290; Indels 12; Gaps 3;

1..595

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Finally, one plasmid amplified cDNA library was made, and 1 million ph were in vivo excised to give plasmid SK1 cDNA plasmids. These steps were performed in the UCI Close Laboratory at the University of California, Riverside (Choi, Close, Fontana). Plasmids were plated and picked at the Clemson University Genomics Institute (CUGI) (Bosham, Palmer, Frisch, Atkins and Ward). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wind, Yu, Frisch, Henry, Simmons, Gates, Kamboj, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of flanking sequence. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.ncbi.nlm.nih.gov/Genbank>. Also see Close LJ, Wind R, Kikvidze A, Wise R (2001) Genetically and physically anchored EST resources for barley genomes. *Barley Genetics Newsletter* 41:29-30. (<http://www.cugl.org/BarleyGeneticsNewsletter/>)

[illegible]


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QY 772 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 831
DB 893 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 952
QY 832 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 891
DB 953 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1012
QY 892 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 951
DB 1013 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1072
QY 952 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1011
DB 1073 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1132
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QY 1072 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1131
DB 1193 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1252
QY 1129 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1188
DB 1252 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1312
QY 1129 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1188
DB 1313 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1372
QY 1249 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1308
DB 1373 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1432
QY 1309 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1368
DB 1433 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1492
QY 1362 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1420
DB 1493 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1552
QY 1411 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1476
DB 1553 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1612
QY 1471 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1539
DB 1613 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 1651

```

RESULT 15

US 09 620 958A 9

Sequence 9, Application US/09620958A

Patent No. 6294338

GENERAL INFORMATION:

APPLICANT: Numura, Kiyotada

TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD

FILE REFERENCE: GPO4-02.0T

CURRENT APPLICATION NUMBER: US/09/620, 958A

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FASTSEQ For Windows Version 3.0

SEQ ID NO 9

LENGTH: 8933

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Sequence of the IAC Bser pseudo target

Patent No. 6294338

NAME/KEY: mutation

LOCATION: (4140)...(4159)

OTHER INFORMATION: Mutated positions: 4140-42, 4145-47, 4152,

OTHER INFORMATION: 4156-57, 4159

US-09-620-958A-9

Query Match 41 89, Score 631.4, DB 4, Length 8933

Best Local Similarity 55.28, Pred. No. 4, Le-89

Matches 849, Conservative 149, Mismatches 511, Indels 30, Gaps 3

QY 1 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 60

DB 113 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 172

QY 61 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 120

DB 173 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 232

QY 121 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 180

DB 233 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 292

QY 181 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 240

DB 293 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 352

QY 241 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 300

DB 413 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 472

QY 354 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 411

DB 473 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 532

QY 413 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 471

DB 533 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 592

QY 473 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 531

DB 593 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 652

QY 532 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 591

DB 653 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 712

QY 592 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 651

DB 713 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 772

QY 652 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 711

DB 773 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 832

QY 712 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 771

DB 833 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 892

QY 772 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 831

DB 893 aatctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 952

QY 832 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 891

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QY 892 atctatcagatgagatcatctctgagctgagacagatctgagagatgacagaccccg 951

The first part of the paper discusses the importance of the study of the history of the United States. It is argued that the study of history is essential for a full understanding of the present. The second part of the paper discusses the importance of the study of the history of the United States. It is argued that the study of history is essential for a full understanding of the present. The third part of the paper discusses the importance of the study of the history of the United States. It is argued that the study of history is essential for a full understanding of the present.

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Run on: July 1, 2002, 13:48:10 ; Search time 56.48.19 seconds

(without alignments)

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Hit list:

Percent Score: 100%

Sequence: 1 at sequence=sequence

Scoring table:

IDENTITY_NUC

Gap 10.0 ; Gap ext 1.0

Sequences: 1797656 seqs, 104629299 residues

Total number of hits satisfying chosen parameters: 4595312

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post processing:

Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_bat *

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

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ALIGNMENTS

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VERSION	AX149648.1
KEYWORDS	GI:14348047
SOURCE	Human immunodeficiency virus
ORGANISM	Human immunodeficiency virus
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AUTHORS	Shao, Y., Wu, R., Wolf, H., and Graf, M.
TITLE	The genome of the HIV-1 subtype (c/v) and use thereof
JOURNAL	Patent: WO 0146614-A 2 25-MAY-2001
GENEAT	Geneat 0088 Gesseltschaft fuer angewandte Biotechnologie (GE)
FEATURES	Shao, Yimou (CN)
source	Location/Qualifiers
BASE COUNT	1026 a 1358 c 1397 g 507 t
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